

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/777,145

Source: _____

Date Processed by STIC: _____

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RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/777,145

TIME: 10:11:54

Input Set : N:\CrF3\RULE60\10777145.raw.txt

Output Set: N:\CRF4\10182004\J777145.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
5     (i) APPLICANT: Schlessinger, Joseph
6         Sap, Jan M.
8     (ii) TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE
9         PHOSPHATASE-ALPHA
11    (iii) NUMBER OF SEQUENCES: 14
13    (iv) CORRESPONDENCE ADDRESS:
14        (A) ADDRESSEE: PENNIE & EDMONDS
15        (B) STREET: 1155 AVENUE OF THE AMERICAS
16        (C) CITY: NEW YORK
17        (D) STATE: NEW YORK
18        (E) COUNTRY: U.S.A.
19        (F) ZIP: 10036
21    (v) COMPUTER READABLE FORM:
22        (A) MEDIUM TYPE: Floppy disk
23        (B) COMPUTER: IBM PC compatible
24        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27    (vi) CURRENT APPLICATION DATA:
C--> 28        (A) APPLICATION NUMBER: US/10/777,145
C--> 29        (B) FILING DATE: 13-Feb-2004
30        (C) CLASSIFICATION:
32    (vii) PRIOR APPLICATION DATA:
W--> 33        (A) APPLICATION NUMBER: US/09/280,597
34        (B) FILING DATE: 29-MAR-1999
W--> 35        (A) APPLICATION NUMBER: US 08/015,985
36        (B) FILING DATE: 10-FEB-1993
38    (viii) ATTORNEY/AGENT INFORMATION:
39        (A) NAME: Coruzzi, Laura A.
40        (B) REGISTRATION NUMBER: 30,742
41        (C) REFERENCE/DOCKET NUMBER: 7683-020
43    (ix) TELECOMMUNICATION INFORMATION:
44        (A) TELEPHONE: (212) 790-9090
45        (B) TELEFAX: (212) 869-9741/8864
46        (C) TELEX: 66141 PENNIE
50 (2) INFORMATION FOR SEQ ID NO: 1:
52     (i) SEQUENCE CHARACTERISTICS:
53         (A) LENGTH: 802 amino acids
54         (B) TYPE: amino acid
55         (D) TOPOLOGY: linear
57     (ii) MOLECULE TYPE: protein
59     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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61 Met Asp Ser Trp Phe Ile Leu Val Leu Leu Gly Ser Gly Leu Ile Cys
62   1           5           10           15
64 Val Ser Ala Asn Asn Ala Thr Thr Val Ala Pro Ser Val Gly Ile Thr
65           20           25           30
67 Arg Leu Ile Asn Ser Ser Thr Ala Glu Pro Val Lys Glu Glu Ala Lys
68           35           40           45
70 Thr Ser Asn Pro Thr Ser Ser Leu Thr Ser Leu Ser Val Ala Pro Thr
71           50           55           60
73 Phe Ser Pro Asn Ile Thr Leu Gly Pro Thr Tyr Leu Thr Thr Val Asn
74   65           70           75           80
76 Ser Ser Asp Ser Asp Asn Gly Thr Thr Arg Thr Ala Ser Thr Asn Ser
77           85           90           95
79 Ile Gly Ile Thr Ile Ser Pro Asn Gly Thr Trp Leu Pro Asp Asn Gln
80           100          105          110
82 Phe Thr Asp Ala Arg Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
83           115          120          125
85 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ser Gly Asn Ser Asp Ser Lys
86           130          135          140
88 Asp Arg Arg Asp Glu Thr Pro Ile Ile Ala Val Met Val Ala Leu Ser
89 145           150          155          160
91 Ser Leu Leu Val Ile Val Phe Ile Ile Ile Val Leu Tyr Met Leu Arg
92           165          170          175
94 Phe Lys Lys Tyr Lys Gln Ala Gly Ser His Ser Asn Ser Phe Arg Leu
95           180          185          190
97 Ser Asn Gly Arg Thr Glu Asp Val Glu Pro Gln Ser Val Pro Leu Leu
98           195          200          205
100 Ala Arg Ser Pro Ser Thr Asn Arg Lys Tyr Pro Pro Leu Pro Val Asp
101           210          215          220
103 Lys Leu Glu Glu Glu Ile Asn Arg Arg Met Ala Asp Asp Asn Lys Leu
104 225           230          235          240
106 Phe Arg Glu Glu Phe Asn Ala Leu Pro Ala Cys Pro Ile Gln Ala Thr
107           245          250          255
109 Cys Glu Ala Ala Ser Lys Glu Glu Asn Lys Glu Lys Asn Arg Tyr Val
110           260          265          270
112 Asn Ile Leu Pro Tyr Asp His Ser Arg Val His Leu Thr Pro Val Glu
113           275          280          285
115 Gly Val Pro Asp Ser Asp Tyr Ile Asn Ala Ser Phe Ile Asn Gly Tyr
116           290          295          300
118 Gln Glu Lys Asn Lys Phe Ile Ala Ala Gln Gly Pro Lys Glu Glu Thr
119 305           310          315          320
121 Val Asn Asp Phe Trp Arg Met Ile Trp Glu Gln Asn Thr Ala Thr Ile
122           325          330          335
124 Val Met Val Thr Asn Leu Lys Glu Arg Lys Glu Cys Lys Cys Ala Gln
125           340          345          350
127 Tyr Trp Pro Asp Gln Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Ser
128           355          360          365
130 Val Glu Asp Val Thr Val Leu Val Asp Tyr Thr Val Arg Lys Phe Cys
131           370          375          380
133 Ile Gln Gln Val Gly Asp Met Thr Asn Arg Lys Pro Gln Arg Leu Ile

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134 385          390          395          400
136 Thr Gln Phe His Phe Thr Ser Trp Pro Asp Phe Gly Val Pro Phe Thr
137          405          410          415
139 Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys Ala Cys Asn Pro
140          420          425          430
142 Gln Tyr Ala Gly Ala Ile Val Val His Cys Ser Ala Gly Val Gly Arg
143          435          440          445
145 Thr Gly Thr Phe Val Val Ile Asp Ala Met Leu Asp Met Met His Thr
146          450          455          460
148 Glu Arg Lys Val Asp Val Tyr Gly Phe Val Ser Arg Ile Arg Ala Gln
149 465          470          475          480
151 Arg Cys Gln Met Val Gln Thr Asp Met Gln Tyr Val Phe Ile Tyr Gln
152          485          490          495
154 Ala Leu Leu Glu His Tyr Leu Tyr Gly Asp Thr Glu Leu Glu Val Thr
155          500          505          510
157 Ser Leu Glu Thr His Leu Gln Lys Ile Tyr Asn Lys Ile Pro Gly Thr
158          515          520          525
160 Ser Asn Asn Gly Leu Glu Glu Glu Phe Lys Lys Leu Thr Ser Ile Lys
161          530          535          540
163 Ile Gln Asn Asp Lys Met Arg Thr Gly Asn Leu Pro Ala Asn Met Lys
164 545          550          555          560
166 Lys Asn Arg Val Leu Gln Ile Ile Pro Tyr Glu Phe Asn Arg Val Ile
167          565          570          575
169 Ile Pro Val Lys Arg Gly Glu Glu Asn Thr Asp Tyr Val Asn Ala Ser
170          580          585          590
172 Phe Ile Asp Gly Tyr Arg Gln Lys Asp Ser Tyr Ile Ala Ser Gln Gly
173          595          600          605
175 Pro Leu Leu His Thr Ile Glu Asp Phe Trp Arg Met Ile Trp Glu Trp
176          610          615          620
178 Lys Ser Cys Ser Ile Val Met Leu Thr Glu Leu Glu Arg Gly Gln
179 625          630          635          640
181 Glu Lys Cys Ala Gln Tyr Trp Pro Ser Asp Gly Leu Val Ser Tyr Gly
182          645          650          655
184 Asp Ile Thr Val Glu Leu Lys Lys Glu Glu Glu Cys Glu Ser Tyr Thr
185          660          665          670
187 Val Arg Asp Leu Leu Val Thr Asn Thr Arg Glu Asn Lys Ser Arg Gln
188          675          680          685
190 Ile Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ser
191          690          695          700
193 Asp Gly Lys Gly Met Ile Ser Ile Ile Ala Ala Val Gln Lys Gln Gln
194 705          710          715          720
196 Gln Gln Ser Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala
197          725          730          735
199 Gly Arg Thr Gly Thr Phe Cys Ala Leu Ser Thr Val Leu Glu Arg Val
200          740          745          750
202 Lys Ala Glu Gly Ile Leu Asp Val Phe Gln Thr Val Lys Ser Leu Arg
203          755          760          765
205 Leu Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys
206          770          775          780

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```

208 Tyr Lys Val Val Gln Glu Tyr Ile Asp Ala Phe Ser Asp Tyr Ala Asn
209 785                790                795                800
211 Phe Lys
214 (2) INFORMATION FOR SEQ ID NO: 2:
216     (i) SEQUENCE CHARACTERISTICS:
217         (A) LENGTH: 2409 base pairs
218         (B) TYPE: nucleic acid
219         (C) STRANDEDNESS: double
220         (D) TOPOLOGY: unknown
222     (ii) MOLECULE TYPE: cDNA
224     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
226 ATGGATTCTT GGTTCATTCT TGTTCCTGCTC GGCAGTGGTC TGATATGTGT CAGTGCCAAC      60
228 AATGCTACCA CAGTTGCACC TTCTGTAGGA ATTACAAGAT TAATTAACCT ATCAACGGCA      120
230 GAACCAGTTA AAGAAGAGGC CAAAACTTCA AATCCAACCT CTCACCTAAC TTCTCTTTCT      180
232 GTGGCACCAA CATTACAGCC AAATATAACT CTGGGACCCA CCTATTTAAC CACTGTCAAT      240
234 TCTTCAGACT CTGACAATGG GACCACAAGA ACAGCAAGCA CCAATTCTAT AGGCATTACA      300
236 ATTTACCAA ATGGAACGTG GCTTCCAGAT AACCAGTTCA CGGATGCCAG AACAGAACCC      360
238 TGGGAGGGGA ATTCCAGCAC CGCAGCAACC ACTCCAGAAA CTTTCCCTCC TTCAGGTAAT      420
240 TCTGACTCGA AGGACAGAAG AGATGAGACA CCAATTATTG CGGTGATGGT GGCCCTGTCC      480
242 TCTCTGCTAG TGATCGTGTT TATTATCATA GTTTTGTACA TGTTAAGGTT TAAGAAATAC      540
244 AAGCAAGCTG GGAGCCATTC CAATTCTTTC CGCTTATCCA ACGGCCGCAC TGAGGATGTG      600
246 GAGCCCCAGA GTGTGCCACT TCTGGCCAGA TCCCCAAGCA CCAACAGGAA ATACCCACCC      660
248 CTGCCCCTGG ACAAGCTGGA AGAGGAAATT AACCAGGAGAA TGGCAGACGA CAATAAGCTC      720
250 TTCAGGGAGG AATTCAACGC TCTCCCTGCA TGTCTTATCC AGGCCACCTG TGAGGCTGCT      780
252 TCCAAGGAGG AAAACAAGGA AAAAAATCGA TATGTAAACA TCTTGCCTTA TGACCACTCT      840
254 AGAGTCCACC TGACACCGGT TGAAGGGGTT CCAGATTCTG ATTACATCAA TGCTTCATTC      900
256 ATCAACGGTT ACCAAGAAAA GAACAAATTC ATTGCTGCAC AAGGACCAAA AGAAGAAACG      960
258 GTGAATGATT TCTGGCGGAT GATCTGGGAA CAAAACACAG CCACCATCGT CATGGTTACC     1020
260 AACCTGAAGG AGAGAAAGGA GTGCAAGTGC GCCCAGTACT GGCCAGACCA AGGCTGCTGG     1080
262 ACCTATGGGA ATATTCGGGT GTCTGTAGAG GATGTGACTG TCCTGGTGGA CTACACAGTA     1140
264 CGGAAGTTCT GCATCCAGCA GGTGGGCGAC ATGACCAACA GAAAGCCACA GCGCCTCATC     1200
266 ACTCAGTTCC ACTTTACCAG CTGGCCAGAC TTTGGGGTGC CTTTACCCC GATCGGCATG     1260
268 CTCAAGTTCC TCAAGAAGGT GAAGGCCTGT AACCCTCAGT ATGCAGGGGC CATCGTGGTC     1320
270 CACTGCAGTG CAGGTGTAGG GCGTACAGGT ACCTTTGTCT TCATTGATGC CATGCTGGAC     1380
272 ATGATGCATA CAGAACGGAA GGTGGACGTG TATGGCTTTG TGAGCCGGAT CCGGGCACAG     1440
274 CGCTGCCAGA TGGTGCAAAC CGATATGCAG TATGTCTTCA TATACCAAGC CCTTCTGGAG     1500
276 CATTATCTCT ATGGAGATAC AGAACTGGAA GTGACCTCTC TAGAAACCCA CCTGCAGAAA     1560
278 ATTTACAACA AAATCCCAGG GACCAGCAAC AATGGATTAG AGGAGGAGTT TAAGAAGTTA     1620
280 ACATCAATCA AAATCCAGAA TGACAAGATG CGGACTGGAA ACCTTCCAGC CAACATGAAG     1680
282 AAGAACCGTG TTTTACAGAT CATTCCATAT GAATTCACAA GAGTGATCAT TCCAGTTAAG     1740
284 CGGGGCGAAG AGAATACAGA CTATGTGAAC GCATCCTTTA TTGATGGCTA CCGGCAGAAG     1800
286 GACTCCTATA TCGCCAGCCA GGGCCCTCTT CTCCACACAA TTGAGGACTT CTGGCGAATG     1860
288 ATCTGGGAGT GGAAATCCTG CTCTATCGTG ATGCTAACAG AACTGGAGGA GAGAGGCCAG     1920
290 GAGAAGTGTG CCCAGTACTG GCCATCTGAT GGACTGGTGT CCTATGGAGA TATTACAGTG     1980
292 GAACTGAAGA AGGAGGAGGA ATGTGAGAGC TACACCGTCC GAGACCTCCT GGTACCAAC     2040
294 ACCAGGGAGA ATAAGAGCCG GCAGATCCGG CAGTTCCACT TCCATGGCTG GCCTGAAGTG     2100
296 GGCATCCCCA GTGACGGAAA GGGCATGATC AGCATCATCG CCGCCGTGCA GAAGCAGCAG     2160
298 CAGCAGTCAG GGAACACCC CATCACCGTG CACTGCAGCG CCGGGGCAGG AAGGACGGGG     2220
300 ACCTTCTGTG CCCTGAGCAC CGTCCTGGAG CGTGTGAAAG CAGAGGGGAT TTTGGATGTC     2280

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302 TTCCAGACTG TCAAGAGCCT GCGGCTACAG AGGCCACACA TGGTCCAGAC ACTGGAACAG      2340
304 TATGAGTTCT GCTACAAGGT GGTGCAGGAG TATATTGATG CATTCTCAGA TTATGCCAAC      2400
306 TTCAAGTAA      2409
309 (2) INFORMATION FOR SEQ ID NO: 3:
311     (i) SEQUENCE CHARACTERISTICS:
312         (A) LENGTH: 793 amino acids
313         (B) TYPE: amino acid
314         (D) TOPOLOGY: linear
316     (ii) MOLECULE TYPE: protein
318     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
320 Met Asp Ser Trp Phe Ile Leu Val Leu Phe Gly Ser Gly Leu Ile His
321   1           5           10           15
323 Val Ser Ala Asn Asn Ala Thr Thr Val Ser Pro Ser Leu Gly Thr Thr
324           20           25           30
326 Arg Leu Ile Lys Thr Ser Thr Thr Glu Leu Ala Lys Glu Glu Asn Lys
327           35           40           45
329 Thr Ser Asn Ser Thr Ser Ser Val Ile Ser Leu Ser Val Ala Pro Thr
330           50           55           60
332 Phe Ser Pro Asn Leu Thr Leu Glu Pro Thr Tyr Val Thr Thr Val Asn
333   65           70           75           80
335 Ser Ser His Ser Asp Asn Gly Thr Arg Arg Ala Ala Ser Thr Glu Ser
336           85           90           95
338 Gly Gly Thr Thr Ile Ser Pro Asn Gly Ser Trp Leu Ile Glu Asn Gln
339           100          105          110
341 Phe Thr Asp Ala Ile Thr Glu Pro Trp Glu Gly Asn Ser Ser Thr Ala
342           115          120          125
344 Ala Thr Thr Pro Glu Thr Phe Pro Pro Ala Asp Glu Thr Pro Ile Ile
345           130          135          140
347 Ala Val Met Val Ala Leu Ser Ser Leu Leu Val Ile Val Phe Ile Ile
348   145          150          155          160
350 Ile Val Leu Tyr Met Leu Arg Phe Lys Lys Tyr Lys Gln Ala Gly Ser
351           165          170          175
353 His Ser Asn Ser Phe Arg Leu Ser Asn Gly Arg Thr Glu Asp Val Glu
354           180          185          190
356 Pro Gln Ser Val Pro Leu Leu Ala Arg Ser Pro Ser Thr Asn Arg Lys
357           195          200          205
359 Tyr Pro Pro Leu Pro Val Asp Lys Leu Glu Glu Glu Ile Asn Arg Arg
360           210          215          220
362 Met Ala Asp Asp Asn Lys Leu Phe Arg Glu Glu Phe Asn Ala Leu Pro
363   225          230          235          240
365 Ala Cys Pro Ile Gln Ala Thr Cys Glu Ala Ala Ser Lys Glu Glu Asn
366           245          250          255
368 Lys Glu Lys Asn Arg Tyr Val Asn Ile Leu Pro Tyr Asp His Ser Arg
369           260          265          270
371 Val His Leu Thr Pro Val Glu Gly Val Pro Asp Ser Asp Tyr Ile Asn
372           275          280          285
374 Ala Ser Phe Ile Asn Gly Tyr Gln Glu Lys Asn Lys Phe Ile Ala Ala
375           290          295          300
377 Gln Gly Pro Lys Glu Glu Thr Val Asn Asp Phe Trp Arg Met Ile Trp

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/777,145

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos.8,12,21,22,24,25,27,28,30,37,39,47,57,72,77,89,94,95,99,104
Seq#:9; Xaa Pos.109,111,115,116,124,125,131,133,135,137,138,139,143,144,153
Seq#:9; Xaa Pos.155,170,174,176,179,180,181,182,183,186,205,211,212,214,215
Seq#:9; Xaa Pos.217,222,227,230,232,240,244,247
Seq#:14; Xaa Pos.10,20,21,22,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38
Seq#:14; Xaa Pos.39,40,41,42,43,55,67,70,87,95,96,97,99,100,103,105,106,112
Seq#:14; Xaa Pos.114,115,116,120,121,123,126,127,128,133,137,138,139,141
Seq#:14; Xaa Pos.143,149,151,182,186,188,195,196,197,198,199,200,201,202
Seq#:14; Xaa Pos.205,209,212,213,214,218,222,224,228,229,244,247,254,257
Seq#:14; Xaa Pos.264,265,266,267

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10777145.raw.txt

Output Set: N:\CRF4\10182004\J777145.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(A) APPLICATION NUMBER:] of (1) (vii)
L:836 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:1142 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14